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ENTEREDCRFIP#25
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1600

RAW SEQUENCE LISTING

DATE: 06/18/2002

PATENT APPLICATION: US/09/558,741

TIME: 07:58:57

Input Set : N:\Crf3\Datahold\EFS\09558741\CIBT-P01-130SequenceListing.txt

Output Set: N:\CRF3\06182002\I558741.raw

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5 <110> APPLICANT: Huston, J.
6   Houston, L.L.
7   Ring, D.
8   Oppermann, H.
10 <120> TITLE OF INVENTION: BIOSYNTHETIC BINDING PROTEINS FOR IMMUNO-TARGETING
12 <130> FILE REFERENCE: CIBT-P01-130
14 <140> CURRENT APPLICATION NUMBER: 09/558,741
15 <141> CURRENT FILING DATE: 2000-04-26
17 <150> PRIOR APPLICATION NUMBER: 07/831,967
18 <151> PRIOR FILING DATE: 1992-02-06
20 <160> NUMBER OF SEQ ID NOS: 16
22 <170> SOFTWARE: PatentIn version 3.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 909
26 <212> TYPE: DNA
27 <213> ORGANISM: Artificial Sequence
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30 <223> OTHER INFORMATION: 741F8 sFv'
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (3)..(752)
35 <223> OTHER INFORMATION:
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40   1           5           10          15
42 cct gga gag aca gtc aag atc tcc tgc aag gct tct ggg tat acc ttc      95
43 Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
44           20           25           30
46 aca aac tat gga atg aac tgg gtg aag cag gct cca gga aag ggt tta      143
47 Thr Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu
48           35           40           45
50 aag tgg atg ggc tgg ata aac acc aac act gga gag cca aca tat gct      191
51 Lys Trp Met Gly Trp Ile Asn Thr Asn Thr Gly Glu Pro Thr Tyr Ala
52           50           55           60
54 gaa gag ttc aag gga cgg ttt gcc ttc tct ttg gaa acc tct gcc agc      239
55 Glu Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser
56           65           70           75
58 act gcc tat ttg cag atc aag aag ctc aaa aat gag gac acg gct aca      287
59 Thr Ala Tyr Leu Gln Ile Lys Lys Leu Lys Asn Glu Asp Thr Ala Thr
60 80           85           90           95
63 tat ttc tgt gga agg caa ttt att acc tac ggc ggg ttt gct aac tgg      335
64 Tyr Phe Cys Gly Arg Gln Phe Ile Thr Tyr Gly Gly Phe Ala Asn Trp

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65 100 105 110
 67 ggc caa ggg act ctg gtc act gtc tct gca tcg agc tcc tcc gga tct 383
 68 Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ser Ser Ser Ser Gly Ser
 69 115 120 125
 71 tca tct agc ggt tcc agc tcg agc gat atc gtc atg acc cag tct cct 431
 72 Ser Ser Ser Gly Ser Ser Ser Ser Asp Ile Val Met Thr Gln Ser Pro
 73 130 135 140
 75 aaa ttc atg tcc acg tca gtg gga gac agg gtc agc atc tcc tgc aag 479
 76 Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Ser Cys Lys
 77 145 150 155
 79 gcc agt cag gat gtg agt act gct gta gcc tgg tat caa caa aaa cca 527
 80 Ala Ser Gln Asp Val Ser Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro
 81 160 165 170 175
 83 ggg caa tct cct aaa cta ctg att tac tgg aca tcc acc cgg cac act 575
 84 Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr
 85 180 185 190
 87 gga gtc cct gat cgc ttc aca ggc agt gga tct ggg aca gat tat act 623
 88 Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Tyr Thr
 89 195 200 205
 91 ctc acc atc agc agt gtg cag gct gaa gac ctg gca ctt cat tac tgt 671
 92 Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Leu His Tyr Cys
 93 210 215 220
 95 cag caa cat tat aga gtg ccg tac acg ttc gga ggg ggg acc aag ctg 719
 96 Gln Gln His Tyr Arg Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu
 97 225 230 235
 99 gag ata aaa cgg gct gat ggg gga ggt gga tgt taacggggga ggtggatgtt 772
 100 Glu Ile Lys Arg Ala Asp Gly Gly Gly Cys
 101 240 245 250
 103 ggggtctcggtt acgttgccga tctcgagget atctttacta actctttaccg taaagttctg 832
 105 gctcaactgt ctgcacgcaa gcttttgcag gatattcatga gcgcttaaga tccgtcgacc 892
 107 tgcaggcatg caagctt 909
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 111 <211> LENGTH: 250
 112 <212> TYPE: PRT
 113 <213> ORGANISM: Artificial Sequence
 115 <220> FEATURE:
 116 <223> OTHER INFORMATION: 741F8 sFv'
 118 <400> SEQUENCE: 2
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 121 1 5 10 15
 125 Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
 126 20 25 30
 129 Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys
 130 35 40 45
 133 Trp Met Gly Trp Ile Asn Thr Asn Thr Gly Glu Pro Thr Tyr Ala Glu
 134 50 55 60
 137 Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr
 138 65 70 75 80
 141 Ala Tyr Leu Gln Ile Lys Lys Leu Lys Asn Glu Asp Thr Ala Thr Tyr

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142          85          90          95
145 Phe Cys Gly Arg Gln Phe Ile Thr Tyr Gly Gly Phe Ala Asn Trp Gly
146          100          105          110
149 Gln Gly Thr Leu Val Thr Val Ser Ala Ser Ser Ser Ser Gly Ser Ser
150          115          120          125
153 Ser Ser Gly Ser Ser Ser Ser Asp Ile Val Met Thr Gln Ser Pro Lys
154          130          135          140
157 Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Ser Cys Lys Ala
158 145          150          155          160
161 Ser Gln Asp Val Ser Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly
162          165          170          175
165 Gln Ser Pro Lys Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly
166          180          185          190
169 Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu
170          195          200          205
173 Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Leu His Tyr Cys Gln
174          210          215          220
177 Gln His Tyr Arg Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu
178 225          230          235          240
181 Ile Lys Arg Ala Asp Gly Gly Gly Gly Cys
182          245          250

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185 <210> SEQ ID NO: 3

186 <211> LENGTH: 779

187 <212> TYPE: DNA

188 <213> ORGANISM: Artificial Sequence

190 <220> FEATURE:

191 <223> OTHER INFORMATION: 26-10 sFv'

W--> 192 <220> FEATURE:

193 <221> NAME/KEY: CDS

194 <222> LOCATION: (3)..(758)

195 <223> OTHER INFORMATION:

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201   1          5          10          15
203 ggc gcc tct gtg cgc atg tcc tgc aaa tcc tct ggg tac att ttc acc      95
204 Gly Ala Ser Val Arg Met Ser Cys Lys Ser Ser Gly Tyr Ile Phe Thr
205          20          25          30
207 gac ttc tac atg aat tgg gtt cgc cag tct cat ggt aag tct cta gac      143
208 Asp Phe Tyr Met Asn Trp Val Arg Gln Ser His Gly Lys Ser Leu Asp
209          35          40          45
211 tac atc ggg tac att tcc cca tac tct ggg gtt acc ggc tac aac cag      191
212 Tyr Ile Gly Tyr Ile Ser Pro Tyr Ser Gly Val Thr Gly Tyr Asn Gln
213          50          55          60
215 aag ttt aaa ggt aag gcg acc ctt act gtc gac aaa tct tcc tca act      239
216 Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr
217          65          70          75
219 gct tac atg gag ctg cgt tct ttg acc tct gag gac tcc gcg gta tac      287
220 Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr

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221 80                               85                               90                               95
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224 Tyr Cys Ala Gly Ser Ser Gly Asn Lys Trp Ala Met Asp Tyr Trp Gly
225                               100                               105                               110
227 cat ggt gct agc gtt act gtg agc tcc tcc gga tct tca tct agc ggt      383
228 His Gly Ala Ser Val Thr Val Ser Ser Ser Gly Ser Ser Ser Ser Gly
229                               115                               120                               125
231 tcc agc tcg agt gga tcc gac gtc gta atg acc cag act ccg ctg tct      431
232 Ser Ser Ser Ser Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser
233                               130                               135                               140
235 ctg ccg gtt tct ctg ggt gac cag gct tct att tct tgc cgc tct tcc      479
236 Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser
237                               145                               150                               155
239 cag tct ctg gtc cat tct aat ggt aac act tac ctg aac tgg tac ctg      527
240 Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu Asn Trp Tyr Leu
241 160                               165                               170                               175
243 caa aag gct ggt cag tct ccg aag ctt ctg atc tac aaa gtc tct aac      575
244 Gln Lys Ala Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn
245                               180                               185                               190
247 cgc ttc tct ggt gtc ccg gat cgt ttc tct ggt tct ggt tct ggt act      623
248 Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
249                               195                               200                               205
251 gac ttc acc ctg aag atc tct cgt gtc cag gcc gaa gac ctg ggt atc      671
252 Asp Phe Thr Leu Lys Ile Ser Arg Val Gln Ala Glu Asp Leu Gly Ile
253                               210                               215                               220
255 tac ttc tgc tct cag act act cat gta ccg ccg act ttt ggt ggt ggc      719
256 Tyr Phe Cys Ser Gln Thr Thr His Val Pro Pro Thr Phe Gly Gly Gly
257                               225                               230                               235
259 acc aag ctc gag att aaa cgt tcc ggg gga ggt gga tgt taactgcagc      768
260 Thr Lys Leu Glu Ile Lys Arg Ser Gly Gly Gly Gly Cys
261 240                               245                               250
263 ccgggggatc c      779
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268 <212> TYPE: PRT
269 <213> ORGANISM: Artificial Sequence
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274 <400> SEQUENCE: 4
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280 Ala Ser Val Arg Met Ser Cys Lys Ser Ser Gly Tyr Ile Phe Thr Asp
281                               20                               25                               30
284 Phe Tyr Met Asn Trp Val Arg Gln Ser His Gly Lys Ser Leu Asp Tyr
285                               35                               40                               45
288 Ile Gly Tyr Ile Ser Pro Tyr Ser Gly Val Thr Gly Tyr Asn Gln Lys
289                               50                               55                               60
292 Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala
293 65                               70                               75                               80

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296 Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr
297                               85                               90                               95
300 Cys Ala Gly Ser Ser Gly Asn Lys Trp Ala Met Asp Tyr Trp Gly His
301                               100                              105                              110
304 Gly Ala Ser Val Thr Val Ser Ser Ser Gly Ser Ser Ser Ser Gly Ser
305                               115                              120                              125
308 Ser Ser Ser Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu
309                               130                              135                              140
312 Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln
313 145                               150                               155                               160
316 Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu Asn Trp Tyr Leu Gln
317                               165                               170                               175
320 Lys Ala Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg
321                               180                              185                              190
324 Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
325                               195                              200                              205
328 Phe Thr Leu Lys Ile Ser Arg Val Gln Ala Glu Asp Leu Gly Ile Tyr
329                               210                              215                              220
332 Phe Cys Ser Gln Thr Thr His Val Pro Pro Thr Phe Gly Gly Gly Thr
333 225                               230                              235                              240
336 Lys Leu Glu Ile Lys Arg Ser Gly Gly Gly Gly Cys
337                               245                              250
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341 <211> LENGTH: 739
342 <212> TYPE: DNA
343 <213> ORGANISM: Artificial Sequence
344 <220> FEATURE:
345 <223> OTHER INFORMATION: 520C9 sFv
346 <220> FEATURE:
347 <221> NAME/KEY: CDS
348 <222> LOCATION: (1)..(729)
349 <223> OTHER INFORMATION:
350 <400> SEQUENCE: 5
355 gag atc caa ttg gtg cag tct gga cct gag ctg aag aag cct gga gag      48
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357 1                               5                               10                               15
359 aca gtc aag atc tcc tgc aag gct tct gga tat acc ttc gca aac tat      96
360 Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ala Asn Tyr
361                               20                               25                               30
363 gga atg aac tgg atg aag cag gct cca gga aag ggt tta aag tgg atg      144
364 Gly Met Asn Trp Met Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
365                               35                               40                               45
367 ggc tgg ata aac acc tac act gga cag tca aca tat gct gat gac ttc      192
368 Gly Trp Ile Asn Thr Tyr Thr Gly Gln Ser Thr Tyr Ala Asp Asp Phe
369                               50                               55                               60
373 aag gaa cgg ttt gcc ttc tct ttg gaa acc tct gcc acc act gcc cat      240
374 Lys Glu Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Thr Thr Ala His
375 65                               70                               75                               80
377 ttg cag atc aac aac ctc aga aat gag gac tcg gcc aca tat ttc tgt      288

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VERIFICATION SUMMARY

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